

Appendix I: Alignment of AAC50763 and SEQ ID NO: 27 of Umezawa et al.

BLASTP 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

RID: E47D8T1E114

Query= gi|1561728|gb|AAC50763.1| transcription factor RTEF-1 [Homo sapiens]
Length=434

Sequences producing significant alignments:	Score (Bits)	E Value
lcl 19493 SID_27	874	0.0

ALIGNMENTS

>lcl|19493 SID_27
Length=427

Score = 874 bits (2258), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 419/427 (98%), Positives = 419/427 (98%), Gaps = 0/427 (0%)

Query	8	ITSNEWSSPTSPEGSTASGGSQALDKPIDNDGEGVWSPDIEQSFQEALAIYPPCGRRKII	67
Sbjct	1	ITSNEWSSPTSPEGSTASGGSQALDKPIDNDAEGVWSPDIEQSFQEALAIYPPCGRRKII	60
Query	68	LSDEGKMYGRNELIARYIKLRTGKTRTRKQVSSHIQVLARRKAREIQAKLKDQAAKDKAL	127
Sbjct	61	LSDEGKMYGRNELIARYIKLRTGKTRTRKQVSSHIQVLARRKAREIQAKLKDQAAKDKAL	120
Query	128	QSMAAMSSAQIISATAFHSSMRLARGPGRPAVSGFWQGALPGQAETSHDVKPFSSQQTAYAV	187
Sbjct	121	QSMAAMSSAQIISATAFHSSMALARGPGRPAVSGFWQGALPGQAGTSHDVKPFSSQQTAYAV	180
Query	188	QPPLPLPGFESPAGPAPSPSAPPAPPWQRRRGSSKLWMLEFSAFLEQQQDPDPTYNKHLF	247
Sbjct	181	QPPLPLPGFESPAGPAPSPSAPPAPPWQGRSSKLWMLEFSAFLEQQQDPDPTYNKHLF	240
Query	248	VHIGQSSPSYLRPYLEAVDIRQIYDKFPEKKGGLKDLFERGPSNAFFLVKFWADLNTNIE	307
Sbjct	241	VHIGQSSPSYSDPYLEAVDIRQIYDKFPEKKGGLKDLFERGPSNAFFLVKFWADLNTNIE	300
Query	308	DEGSSFYGVSSQYESPENMIITCSTKVCSTKQVVEKVETETARYENGHYSYRIHRSPLC	367
Sbjct	301	DEGSSFYGVSSQYESPENMIITCSTKVCSTKQVVEKVETETARYENGHYSYRIHRSPLC	360
Query	368	EYMINFIHKLKHLPEKYMMNSVLENFTILQVVTNRDTQETLLCIAVFEVSASEHGAQHH	427

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Sbjct  361  EYMINFIHKLKHLPEKYYMMNSVLENFTILQVVTNRDTQETLLCIAYVFEVSASEHGAQHH  420
Query  428  IYRLVKE  434
          IYRLVKE
Sbjct  421  IYRLVKE  427
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